

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAQPaiHi: 995 aa
>SEQ ID NO:2
vs /tmp/fastaDAARPaiHi library
searching /tmp/fastaDAARPaiHi library

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, gap-pen: -12/-2, width: 16
Scan time: 0.050

The best scores are: opt
NM_000096 ACCESSION:NM_000096 NID: gi 4557484 ref (1008) 2671

>>NM_000096 ACCESSION:NM_000096 NID: gi 4557484 ref NM_0 (1008 aa)
initn: 1414 init1: 972 opt: 2671
Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)

	10	20	30	40	50	
SEQ	MKILILGIFLFLCSPGWAIDRHCYIGIEESIWNYPSPGKNMLNEKPFSE	DL	----	FLQ		
	:	:	:	:	:	:
NM_000	MKILILGIFLFLCSTPAWAKEKHYYIGIIEETTWDYA	---	SDHGEKKLISVDTEHSNIYLQ			
	10	20	30	40	50	
	60	70	80	90	100	110
SEQ	GGQARKSFVFKKALYFQYTDNTFQRIIEKPSWLGFLGPMIKAETGDFIYVHVKNNASRAY					
	:	:	:	:	:	:
NM_000	NGPDRIGRLYKKALYLYQYTDDETFRITIEKPVWLGLGPIIKAETGDKVYVHLKNLASRPY					
	60	70	80	90	100	110
	120	130	140	150	160	170
SEQ	SYHPHGLTYSKENEAHGAIIYPDNTTGLQKEVEYLEPGKQYTYKQYVEEHQGP	GNDSNCV				
	:	:	:	:	:	:
NM_000	TFHSHGITYYKEHE--GAIIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCV					
	120	130	140	150	160	170
	180	190	200	210	220	230
SEQ	TRIIYSHIDTARDVASGLIGPILTCRGTNLNGDTEKDIDRSSFLMFSTTDESRSWYS	DEN				
	:	:	:	:	:	:
NM_000	TRIIYSHIDAPKDIASGLIGPLIICKKDSLDKEKEKHIDREFVVMFVSVVDENFSWYLEDN					
	180	190	200	210	220	230
	240	250	260	270	280	290
SEQ	IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPNLTMCAEDRVQWYFVGMGGVADIH					
	:	:	:	:	:	:
NM_000	IKTYCSEPEKVKDKDNEDFQESNRMYSVNGYTFGSLPGLSMCAEDRVKWLFGMGNEVDVH					
	240	250	260	270	280	290
	300	310	320	330	340	350
SEQ	PVYLRGQTLISRNHRKDTIMLFPSSLEDAFMVAKAPGVWMLGCQ----	IHESMQAFFKVS				
	:	:	:	:	:	:
NM_000	AAFFHGGQALTINKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQ					
	300	310	320	330	340	350

	360	370	380	390	400	410
SEQ	NCQKPSTEAFVTGTHVIHYIIAAKEILWNYAPSGIDFFTKKNLTAAGSKSQLFFERSPTR					

NM_000	ECNKSSSKDNIRGKHVRHYIIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTR					
	360	370	380	390	400	410
	420	430	440	450	460	
SEQ	IGGTYKKLIYREYTDASFQTQKAR---EEHLGILGPVFKAEVGQTIKITFYNNASLPLSI					

NM_000	IGGSYKKLVYREYTDASFQTNRKERGPEEEHLGILGPVIWAEVGDTIRVTFHNKGAYPLSI					
	420	430	440	450	460	470
	470	480	490	500	510	520
SEQ	QPPGLHYNKSNEGLFYE---TPGG-STPPSSHVSPGTTFFVYTWEVPKDVGPSTDPNCL					

NM_000	EPIGVRFNKNNEGTYYSFNYPNQSRVPPSASHVAPTETFTYEWTPKEVGPTNADPVCL					
	480	490	500	510	520	530
	530	540	550	560	570	580
SEQ	TWFYYSVNGKKDINSGLLGPLLICRNGSLGDDGKQKGVDFYLLATIFDENESNLLDE					

NM_000	AKMYSAVDPTKDIFTGLIGPMKICKKGSLSHANGRQKDVDFYLLFPTVFDENESLLED					
	540	550	560	570	580	590
	590	600	610	620	630	640
SEQ	N-RTFITEPENIDKEDTDCQASNKMYSGINGMYGNLPGDLTCLGDNVLWHVFSVGSVEDL					

NM_000	NIRMFTTAPDQVDKEDDFQESNKMHSNMGFMYGNQPGLTMCCKGDSVVWYLFSAAGNEADV					
	600	610	620	630	640	650
	650	660	670	680	690	700
SEQ	HGIYFSGNTFTSLGARRDTIPMFYTSQTLTLPDSIGTFDLVCMTHHNLGGMKHKYHV					

NM_000	HGIYFSGNTYLWRGERRDANLFPQTSLLHMPDTEGTFNVECLTTDHYTGGMKQKYTV					
	660	670	680	690	700	710
	710	720	730	740	750	760
SEQ	RQCGKPNPDQTYQEEKIIITIAAEEMEWYDYSRQWENELHHLRRENQTSMYVDRSGTL					

NM_000	NQCRQSEDSTFYLGERTYY-IAAVEVEWDYSPQREWEKELHHLQEQNVSNALDKGEFY					
	720	730	740	750	760	770
	770	780	790	800	810	820
SEQ	LGSKYKKVLYRQYDDNTFTNQTKRNEGEKHLGILGILLNPGQIIQIIFKNKAARPYSI					

NM_000	IGSKYKKVVYRQYTDSTFRVPVERKAEHLGILGPQLHADVGDKVKIIFKNMATRPSYI					
	780	790	800	810	820	830
	830	840	850	860	870	880
SEQ	HAHGVKTNNSTVVPTQPGEIQIYTWQIPDRGTSLDFECIPWFYYSTVSVAKDLHSGLV					

NM_000	HAHGVQTESSTVTPLPGETLTYVWKIPERSGAGTEDSACIPWAYYSTVDQVKDLYSGLI					
	840	850	860	870	880	890

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      890      900      910      920      930
SEQ    GPLSVCR----KDINPN-IVHRVLHFMIFDENESWYFEDSINTYASKPNKVDKENDNFQL
      ::: ::: : ::: .. : : : : : : : : : : : : : : : : : : : : : : : :
NM_000  GPLIVCRRPYLKVFNP RRKLEFALLFLVFDENESWYLDDNIKTYS DHPEKVNKDDEEFIE
      900      910      920      930      940      950

      940      950      960      970      980      990
SEQ    SNQMHAINGRLFGNNQGITFHVGDVVNWYLGIGNEADLHTVHFHGH SFYKHKYLI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
NM_000  SNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGH SFQYKHR
      960      970      980      990      1000

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995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:16:31 2002 done: Wed Sep 18 11:16:32 2002

Scan time: 0.050 Display time: 1.417

Function used was FASTA